```
                .         .         .         .         .
  1 GGCACGAGGT CCCCGACGCG CCCCGCCCAA CCCCTACGAT GAAGAGGGCG 50
  1                                         M   K   R   A   4

                .         .         .         .         .
 51 TCCGCTGGAG GGAGCCGGCT GCTGGCATGG GTGCTGTGGC TGCAGGCCTG 100
  5 S   A   G   G     S   R   L     L   A   W     V   L   W   L     Q   A   W  21

                .         .         .         .         .
101 GCAGGTGGCA GCCCCATGCC CAGGTGCCTG CGTATGCTAC AATGAGCCCA 150
 22   Q   V   A     A   P   C   P     G   A   C     V   C   Y     N   E   P   K 38

                .         .         .         .         .
151 AGGTGACGAC AAGCTGCCCC CAGCAGGGCC TGCAGGCTGT GCCCGTGGGC 200
 39     V   T   T     S   C   P     Q   Q   G   L     Q   A   V     P   V   G    54

                .         .         .         .         .
201 ATCCCTGCTG CCAGCCAGCG CATCTTCCTG CACGGCAACC GCATCTCGCA 250
 55 I   P   A   A     S   Q   R     I   F   L     H   G   N   R     I   S   H  71

                .         .         .         .         .
251 TGTGCCAGCT GCCAGCTTCC GTGCCTGCCG CAACCTCACC ATCCTGTGGC 300
 72   V   P   A     A   S   F   R     A   C   R     N   L   T     I   L   W   L 88

                .         .         .         .         .
301 TGCACTCGAA TGTGCTGGCC CGAATTGATG CGGCTGCCTT CACTGGCCTG 350
 89     H   S   N     V   L   A     R   I   D   A     A   A   F     T   G   L   104

                .         .         .         .         .
351 GCCCTCCTGG AGCAGCTGGA CCTCAGCGAT AATGCACAGC TCCGGTCTGT 400
105 A   L   L   E     Q   L   D     L   S   D     N   A   Q   L     R   S   V  121

                .         .         .         .         .
401 GGACCCTGCC ACATTCCACG GCCTGGGCCG CCTACACACG CTGCACCTGG 450
122   D   P   A     T   F   H   G     L   G   R     L   H   T     L   H   L   D 138

                .         .         .         .         .
451 ACCGCTGCGG CCTGCAGGAG CTGGGCCCGG GGCTGTTCCG CGGCCTGGCT 500
139     R   C   G     L   Q   E     L   G   P   G     L   F   R     G   L   A   154

                .         .         .         .         .
501 GCCCTGCAGT ACCTCTACCT GCAGGACAAC GCGCTGCAGG CACTGCCTGA 550
155 A   L   Q   Y     L   Y   L     Q   D   N     A   L   Q   A     L   P   D  171

                .         .         .         .         .
551 TGACACCTTC CGCGACCTGG GCAACCTCAC ACACCTCTTC CTGCACGGCA 600
172   D   T   F     R   D   L   G     N   L   T     H   L   F     L   H   G   N 188
```

FIG. 1A

```
                .         .         .         .         .
601 ACCGCATCTC CAGCGTGCCC GAGCGCGCCT TCCGTGGGCT GCACAGCCTC 650
189   R I S   S V P   E R A F   R G L   H S L   204

                .         .         .         .         .
651 GACCGTCTCC TACTGCACCA GAACCGCGTG GCCCATGTGC ACCCGCATGC 700
205 D R L L   L H Q   N R V   A H V H   P H A   221

                .         .         .         .         .
701 CTTCCGTGAC CTTGGCCGCC TCATGACACT CTATCTGTTT GCCAACAATC 750
222  F R D   L G R L   M T L   Y L F   A N N L 238

                .         .         .         .         .
751 TATCAGCGCT GCCCACTGAG GCCCTGGCCC CCCTGCGTGC CCTGCAGTAC 800
239   S A L   P T E   A L A P   L R A   L Q Y   254

                .         .         .         .         .
801 CTGAGGCTCA ACGACAACCC CTGGGTGTGT GACTGCCGGG CACGCCCACT 850
255 L R L N   D N P   W V C   D C R A   R P L 271

                .         .         .         .         .
851 CTGGGCCTGG CTGCAGAAGT TCCGCGGCTC CTCCTCCGAG GTGCCCTGCA 900
272  W A W   L Q K F   R G S   S S E   V P C S 288

                .         .         .         .         .
901 GCCTCCCGCA ACGCCTGGCT GGCCGTGACC TCAAACGCCT AGCTGCCAAT 950
289   L P Q   R L A   G R D L   K R L   A A N   304

                .         .         .         .         .
951 GACCTGCAGG GCTGCGCTGT GGCCACCGGC CCTTACCATC CCATCTGGAC 1000
305 D L Q G   C A V   A T G   P Y H P   I W T 321

                .         .         .         .         .
1001 CGGCAGGGCC ACCGATGAGG AGCCGCTGGG GCTTCCCAAG TGCTGCCAGC 1050
322  G R A   T D E E   P L G   L P K   C C Q P 338

                .         .         .         .         .
1051 CAGATGCCGC TGACAAGGCC TCAGTACTGG AGCCTGGAAG ACCAGCTTCG 1100
339   D A A   D K A   S V L E   P G R   P A S   354

                .         .         .         .         .
1101 GCAGGCAATG CGCTGAAGGG ACGCGTGCCG CCCGGTGACA GCCCGCCGGG 1150
355 A G N A   L K G   R V P   P G D S   P P G 371

                .         .         .         .         .
1151 CAACGGCTCT GGCCCACGGC ACATCAATGA CTCACCCTTT GGGACTCTGC 1200
372  N G S   G P R H   I N D   S P F   G T L P 388
```

FIG. 1B

```
                .         .         .         .         .
1201 CTGGCTCTGC TGAGCCCCCG GCTCACTGCA GTGCGGCCCG AGGGCTCCGA 1250
 389   G  S  A   E  P  P   A  H  C  S   A  A  R   G  L  R   404

                .         .         .         .         .
1251 GCCACCAGGT TCCCCACTTC GGGCCCTCGC CGGAGGCCAG GCTGTTCACG 1300
 405 A  T  R  F   P  T  S   G  P  R   R  R  P  G   C  S  R  421

                .         .         .         .         .
1301 CAAGAACCGC ACCCGCAGCC ACTGCCGTCT GGGCCAGGCA GGCAGCGGGG 1350
 422  K  N  R   T  R  S  H   C  R  L   G  Q  A   G  S  G  G 438

                .         .         .         .         .
1351 GTGGCGGGAC TGGTGACTCA GAAGGCTCAG GTGCCCTACC CAGCCTCACC 1400
 439   G  G  T   G  D  S   E  G  S  G   A  L  P   S  L  T   454

                .         .         .         .         .
1401 TGCAGCCTCA CCCCCCTGGG CCTGGCGCTG GTGCTGTGGA CAGTGCTTGG 1450
 455 C  S  L  T   P  L  G   L  A  L   V  L  W  T   V  L  G  471

                .         .         .         .         .
1451 GCCCTGCTGA CCCCCAGCGG ACACAAGAGC GTGCTCAGCA GCCAGGTGTG 1500
 472  P  C  *                                              473

                .         .         .         .         .
1501 TGTACATACG GGGTCTCTCT CCACGCCGCC AAGCCAGCCG GGCGGCCGAC 1550

                .         .         .         .         .
1551 CCGTGGGGCA GGCCAGGCCA GGTCCTCCCT GATGGACGCC TGCCGCCCGC 1600

                .         .         .         .         .
1601 CACCCCCATC TCCACCCCAT CATGTTTACA GGGTTCGGCG GCAGCGTTTG 1650

                .         .         .         .         .
1651 TTCCAGAACG CCGCCTCCCA CCCAGATCGC GGTATATAGA GATATGCATT 1700

                .         .         .         .         .
1701 TTATTTTACT TGTGTAAAAA TATCGGACGA CGTGGAATAA AGAGCTCTTT 1750

                .         .
1751 TCTTAAAAAA AAAAAAAAAA AACTCGA 1777
```

FIG. 1C

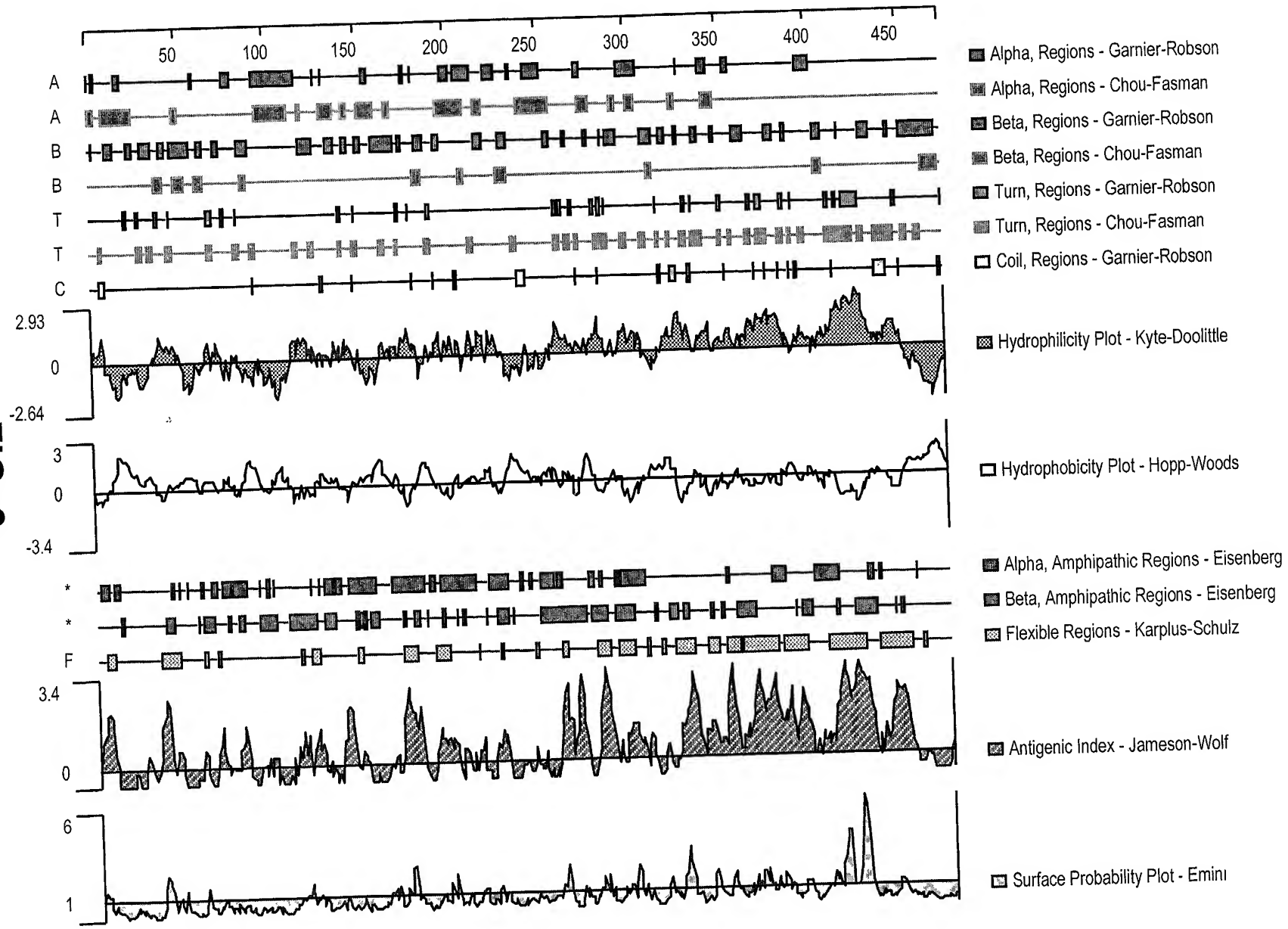
50
100
150
200
250
300
350
400
450
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
2.93
0
-2.64
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
*
*
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini

FIG. 2